

FIGURE 25

GTCTTCCCTTGTCTCTCGCGCCAGTCTCTCTCCCTGGTGTCTCTCAGCCGCTGTGCGAGGAGAGACCCCGA
 GACCGGGCTGCAGTCTCGCGGGCTTCTCCCGCTGGGGGGCTCTCCGCTCGGCGAGTGTCTGAGCGCCCTTAG
 AGCTCTCCCTTTCGCGCTCCCTCTCTCTCGCGCGCGCAGCAGTGCACATCGGGTGTGTGGAGGTAGATGGGCTCCG
 GCCCGGAGGCGCGGTGGATCGCGCTCGGCGCTGGGCGAGAGCAGCGCGATTCAGCTGCCCGCGCGCCCGCGGATC
 CCCCTGCGAGTCCCCGGTTACGCCATCGGGACCTCTCGAGCAGCAGCACCGCCCTCGCCTCTCTGAGCGGATC
 GCCCGCGAGGCCAGCAGCAGATGATCGCGGGTCCCTTCTCTGCTTGGATTCTTAGCACCACACAGCTCAG
 CAGAAACAGAGGCTCCGAATCTCATTGGGCACATCCGCCATGTGACCGGTGCCACCGCGCAGGTGCTAAOCTGT
 GACAGTGTCTCAGCAGGAACCTATGTCTCTGAGCATTGTACCAACACAAGCGTCTGCGGTCTGACAGCAGTGTCCCT
 GTGGGACCTTTACCGAGCATGAGAAATGGCATAGAGAAATGCCATGACTGTAGTCAGCCATGCCCCATGGCCAAATG
 ATTGAGAAATTACCTTGTCTGCTCTGACTGACCGAGAAATGCATTTGCCCACTTGCATGTTCAGTCTAACGCT
 ACCTGTGCCCCCCTACGCTGTGTCTCTGGGTGGGGTGTGCGGAAGAAAGGACAGAGACTGAGGATGTGCGG
 TGTAAAGCAGTGTGCTCGGGTACCTTCTCAGATGTGCCTTCTAGTGTGATGAAATGCAAGACATACACAGACTGT
 CTGAGTCAGAACCTGTGTGATCAAGCCGGGACCAAGGAGACAGACAACGTCTGTGGCACACTCCGCTCTCTC
 TCCAGCTCCACCTCACCTTCCCTGGCACAGCCATCTTCCAGCCCTGAGCACATGGAACCCATGAAGTCCCT
 TCCTCCACTTATGTTCCCAAAGGCATGAACCTCAACAGAAATCCAACCTTCTGCTCTGTGTAGACCAAGGTAAGT
 AGTAGCATCCAGGAAGGACAGTCCCTGACACACAAGCTCAGCAAGGGGGAAGGAAAGCTGAAACAAGACCTC
 CCAACCTTTCAGGTAGTCAACACACAGCAAGGCCCCACACAGACACATCTTGAAGCTGCTGCCCTTCATGGAG
 GCCATGTGGGGCGAGAAGTCCAGCACGCCCATCAAGGGCCCCAAGAGGGGACATCTTAGACAGAACTACACAGG
 CATTTTGACATCAATGAGCATTGCGCTGGATGATGTGCTTTTCTGCTGCTGTGTGCTTGTGGTGAATGTGGT
 TGCAGTATCCGAAAAGCTCGAGGACTCTGAAAAGGGGCCCGGAGGATCCAGTGCCTATGTGGAAAGGCA
 GGGCTGAAGAAATCCATGACTCCAAACCCAGAAACCGGGAAGAAATGGATCTACTACTGCAATGGCCATGATGAT
 ATCTCTGAAGCTGTAGCAGCCCAAGTGGGAAGCCAGTGGAAAGATATCTACAGTCTTTTTCGAGTCCGAGTGAAG
 AGGGAGGTGCTGCTTTCTCCAAATGGGTACACAGCCGACCAAGCGGGCTCAGCGAGCTCTGCAGCATCGGACC
 ATCCGGGGCCCCGAGGCCAGCTCGCCAGCTAATTAGCGCCCTGCGCCAGCAGCCGGAACGATGTTGTGGAG
 AAGATTCTGGGCTGATGGAGAACAACACCCAGCTGGAAATGCAAACTAGCTCTCCGATGAGCCAGCCCGC
 CTTAGCCGAGGCCATCCCCAGCCCAACCGGAAACTTGAGAAATTCGCTCTCTGACGCTGAGCGCTTCCCCA
 CAGGACAGAAGCAAGGCTTCTTCTGGATGAGTGGAGCCCTTCCGCTGTGACTCTGCTCAGCGCTCC
 TCCGCTCTGAGCAGGAACGGTTCCTTTATTACCAAGAAAGAGGACACAGTGTGGCGAGGTACGCTGAG
 CCTGTGACTCTGAGCTATCTTTATGATGACATGCTCCACTTCTAAATCTGAGAGCTCGGGTGAATGAAGAG
 ATTCCCGAGGCTGAGGACAACTAGACCGGCTATTTCGAATTTATTGAGTCAAGAGCCAGGAGCCAGCCGAGCC
 CTCTCGGACTCTGTTTATAGCCATCTTCTGACCTGCTGTAGACATAGGGATACGTCAATCTCTGGAATTAATCA
 ATTCTAGTGCAGGGTGGTTTTTAAATTTCTCTGTTTTCTGATTTTTTGTGTTGGGGTGTGTGTGTGTTTTGT
 GT
 TCTCTCTCTTTTTTTTTTAAATAAATCTCTCGGGAAGTGTGTTTATAAGCCTTTCGACAGGTGAATCTGTGTGAA
 ATACCCACACATAAAGTTTTTAAAGTCCATATTTCTCCATTTTGCCTCTCTATGATTTTCAAGATTATTCTGT
 TGCATTTAAATTTACTTAACTTACCATAAATGCAAGTGTGACTTTTCCACACACTGGAATGTGAGGCTCTTAAC
 TCTTAAAAAGTATAATGGCATCTTGTGAATCTATAAGCAGTCTTATGTCTCTTAAACATTACACCTACTTTTT
 AAAAAACAATATATTACTATTTTATTATTGTTTGTCTTTTATAAATTTCTTAAAGATTAAAGAAATTAAGA
 CCCCATTGAGTTACTGTATGCAATCAACTTTGAGTTATCTTTTAAATATGTCTTGTATAGTTTCAATATCATG
 CTGAAATCTGACCACTATTGCTGATTGTATGTTTTTACCTGGGACCGGTGTAAGTCTGTATTACTTGTATC
 TCTTTCTATGTATATGCTCTGGGCTGGGAGAAATGAAATCCTCAAGCCTACAGGATTTGCTATTTAAGTGGCT
 GACAACTGGGGCCACCAAGAACTTGAACCTTACCTTTTAGGATTTGAGCTGTCTGGAACACATTGCTGCACTTT
 GGAAGTCAAAATCAAGTGCAGTGGCGCCCTTCCATAGAGAAATTTGCCCGACTTGTCTTTAAAGATGTCTGT
 TTTTATATACATAAATCAATGAGTCCCAATCTGCTCTCAAGGCTGTGCTGCTGGGATTCCTTCAACAAAT
 ACTTTAAATAAAAATGCTGCAACTGTAAAGACCTTGTCTGATATATTGCAACTATGTCTCCCATTTTCAAAATG
 TACCTTTAAAGTGTGAGCTGTGCTGAGTTCCCAATGCAAGGTGGCGTGAATCCCTTTGTGTGGGTGGGTGTGAG
 GTAGTGGTGAAGGACCGATATCAGAAAAATGCTTCAAGTGTACTAATTTTAAATAAACATTAGGTGTTTGTGTA
 AAAAAAAA

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FIGURE 26

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52594

><subunit 1 of 1, 655 aa, 1 stop

><MW: 71845, pI: 8.22, NX(S/T): 8

MGTSPSSSTALASCRIARRATATMIAGSLLLLGFLSTTTAQPEQKASNLIGTYRHHVDRATG
QVLTCDKCPAGTYVSEHCTNTSLRVCSSCPVGTFTTRHENGIEKCHDCSQPCPWPMIEKLP
ALTDRECTCPPGMFQSNATCAPHTVCPVGVGVRKKGTETEDVRCKQCARGTFSDVPSSVMKC
KAYTDCLSQNLVVIKPGTKETDNVCGTLPSSFSSSTSPSPGTAIFPRPEHMETHEVPSSTYVP
KGMNSTESNSSASVRPKVLSSIQEGTVPDNTSSARGKEDVNKTLPLNLQVNVHQQGPHRRHIL
KLLPSMEATGGEKSSTPIKGPKRGHPRQNLHKHFDINEHLPWMIVLFLLLVLVVIVVCSIRK
SSRTLKKGPRQDPSAIVEKAGLKKSMPTPTQNRKWIYYCNGHGIDILKLVAQVGSQWKDIY
QFLCNASEREVAAFSNGYTADHERAYALQHWTIRGPEASLAQLISALRQHRNDVVEKIRG
LMEDTTQLETDKLALPMSPLSPSPFIPSPNAKLENSALLTVEPSQDKNKGGFFVDESEPLL
RCDSTSSGSSALSRNGSFITKEKKDTVLRQVRLDPCDLQPIFDDMLHFLNPEELRVIEEIPQ
AEDKLDRLFEIIGVKSQEASQTLLDSVYSHLPDLL

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 350-370

FIGURE 27

ATGGGAAGCCAGTAACACTGTGGCCTACTATCTCTCCGTGGTGGCCATCTACATTTTTGGGA
CTCGGGAATTATGAGGTAGAGGTGGAGGCGGAGCCGGATGTCAGAGGTCCTGAAATAGTCAC
CATGGGGGAAAAATGATCCGCTTGCTGTTGAAGCCCCCTTCTCATCCGATCGCTTTTGGCC
TTGATGATTTTGAAATAAGTCTCTGTGTCACCAGATGCAGATGCTGTTGCTGCACAGATCCTG
TCACTGCTGCCATTGAAGTTTTTCCAAATCATCGTCATTGGGATCATTGCATTGATATTAGC
ACTGGCCATTGGTCTGGGCATCCACTTCGACTGCTCAGGGGAAGTACAGATGTCGCTCATCCT
TTAAGTGTATCGAGCTGTAGCTCGATGTGACGAGTCTCGGATTGCAAGAGCGGGGAGGAC
GAGTACCGCTGTGTCGGGTGGTGGTCAGAAATGCCGTGCTCCAGGTGTTTCACAGCTGCTTC
GTGGAAGACCATGTGCTCCGATGACTGGAAGGGTCACTACGCAAAATGTTGCCTGTGCCAAC
TGGGTTTCCCAAGCTATGTGAGTTCAGATAAACCTCAGAGTGAGCTCGCTGGAGGGGCGAGTTC
CGGGAGGAGTTTGTGTCCATCGATCACCTCTTGCCAGATGACAAGGTGACTGCATTACACCA
CTCAGTATATGTGAGGGAGGGATGTGCCTCTGGCCACGTGGTTACCTTGCAGTGCACAGCCT
GTGGTCATAGAAGGGGCTACAGCTCACGCATCGTGGGTGGAACATGTCTTGTCTCTCGCAG
TGGCCCTGGCAGGCCAGCCTTCACTTCCAGGGCTACCACTGTGCGGGGGCTCTGTATCAC
GCCCTGTGGATCATCACTGTGCACACTGTGTTTATGACTTGTACCTCCCAAGTCATGGA
CCATCCAGGTGGGTCTAGTTTCCCTGTTGGACAATCCAGCCCCATCCCACTTGGTGGAGAAG
ATTGTCTACCACAGCAAGTACAAGCCAAAGAGGCTGGGCAATGACATGCCCTTATGAAGCT
GGCCGGGCCACTCACGTTCAATGAAATGATCCAGCCTGTGTGCTGCCAACTCTGAAGAGA
ACTTCCCCGATGGAAGAGTGTGCTGGACGTGAGGATGGGGGGCCACAGAGGATGGAGGTGAC
GCCTCCCCTGTCTGAACCAGCGCGGCCCTCCCTTTGATTTCACCAAGATCTGCAACCACAG
GGACGTGTACGTTGGCATCATCTCCCCCTCCATGCTCTGCGCGGGCTACCTGACGGGTGGCG
TGGAAGCTGCCAGGGGGACAGCGGGGGCCCCCTGGTGTGTCAAGAGAGGAGGCTGTGGAAG
TTAGTGGGAGCGACAGCTTTGGCATCGGCTGCGCAGAGGTGAACAAGCCTGGGGTGTACAC
CCGTGTCACTCCTTCTGGACTGGATCCACGAGCAGATGGAGAGAGACCTAAAAACCTGA
GAGGAAGGGGCAAGTAGCCACCTGAGTTCCTGAGGTGATGAAGACAGCCCATGCTCCCT
GGACTCCCGTGTAGGAACCTGCACACGAGCAGACACCTTGGAGCTCTGAGTTCGGGCACCA
GTAGCAGGCCCGAAAGAGGCACCTTCCATCTGATTCCAGCACAACTTCAAGCTGCTTTTT
GTTTTTTGTTTTTTGAGGTGGAGTCTCGCTCTGTGTCACAGGCTGGAGTGCAGTGGCGAAA
TCCCTGCTCACTGCAGCCTCCGCTTCCCTGGTTCAAGCGATTCTCTTGCTCAGCTTCCCCA
GTAGCTGGGACCACAGGTGCCCGCCACCACACCACTAATTTTTGTATTTTTAGTAGAGAC
AGGGTTTACCATGTTGGCCAGGCTGCTCTCAAACCCCTGACCTCAAATGATGTGCTGCTT
CAGCCTCCACAGTGTGGGATTACAGGCATGGGCCACACGCGCTAGCCTCAGCTCCTTTTC
TGATCTTCACTAAGAACAAAAGAAGCAGCAACTTGCAAGGGCGGCTTTCCCACTGGTCCAT
CTGGTTTTCTCTCCAGGGTCTTGCAAAATTCCTGACGAGATAAGCAGTTATGTGACCTCAG
TGCAAGGCCACCAACAGCCACTCAGAAAAGACGCACACGCCACAGTGCAGAACTGCAGT
ACTGCACGTTTTATCTTAGGGACACAGAACCAACCCACCTTCTACTTCCAAGACTTAT
TTTCATGTTGGGGAGTTAATCTAGGAATGACTCGTTTAAAGGCTATTTTCATGATTCTT
TGTAGCATTTGGTGTCTGACGTATTATGTCTTTGATTCCAAATAATATGTTTCTCCCT
CATTTGCTGGCGTGTCTGCGTGGACTGGTGACGTGAATCAAAATCATCCACTGAAA

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